SEQUENCE LISTING

<110> Slamon, Dennis J.
Anderson, Lee A.
Ginther, Charles L.
The Regents of the University of California

<120> Amplified and Overexpressed Gene in Colorectal Cancers

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<140> US 10/539,868
<141> 2005-06-16

<150> US 10/346,367
<151> 2003-01-15

<150> WO PCT/US04/01153
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<170> PatentIn Ver. 2.1

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Val Ala Cys Glu Leu Gly Arg Leu Tyr Asn Lys Asp Ala Val Ile Glu
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Phe Leu Leu Asp Lys Ser Ala Glu Lys Ala Leu Gly Lys Ala Ala Ser
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His Ile Lys Ser Ile Lys Asn Val Thr Glu Leu Lys Leu Ser Asp Asn
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Pro Ala Trp Glu Gly Asp Lys Gly Asn Thr Lys Gly Asp Lys His Asp
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Asp Leu Gln Arg Ala Arg Phe Ile Cys Pro Val Val Gly Leu Glu Met
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Gly Ala Ala Phe Gln Glu Asp Asp Val Ile Val Leu Asn Gly Thr Lys
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Glu Asp Val Asp Val Leu Lys Thr Arg Met Glu Glu Arg Arg Leu Arg
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Ala Lys Leu Glu Lys Lys Thr Lys Lys Pro Lys Ala Ala Glu Ser Val
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Arg Val Arg Asn Cys Ser Ser Pro Glu Phe Ser Lys Thr Leu Gln Leu
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Ile Asp Asn Lys Thr Pro Glu Leu Arg Asp Asp Asp Phe Leu Gly Gly
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Ala Glu Cys Ser Leu Gly Gln Ile Val Ser Ser Gln Val Leu Thr Leu
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Pro Leu Met Leu Lys Pro Gly Lys Pro Ala Gly Arg Gly Thr Ile Thr
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Val Ser Ala Gln Glu Leu Lys Asp Asn Arg Val Val Thr Met Glu Val
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Glu Ala Arg Asn Leu Asp Lys Lys Asp Phe Leu Gly Lys Ser Asp Pro
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Phe Leu Glu Phe Phe Arg Gln Gly Asp Gly Lys Trp His Leu Val Tyr
165 170 175

Arg Ser Glu Val Ile Lys Asn Asn Leu Asn Pro Thr Trp Lys Arg Phe
180 185 190

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195 200 205

Gln Val Gln Cys Ser Asp Tyr Asp Ser Asp Gly Ser His Asp Leu Ile
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Gly Thr Phe His Thr Ser Leu Ala Gln Leu Gln Ala Val Pro Ala Glu
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Phe Glu Cys Ile His Pro Glu Lys Gln Gln Lys Lys Lys Ser Tyr Lys
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Ile Gln Gly Ile Val Asp Ala Tyr Arg Gln Ala Leu Pro Gln Val Arg
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Leu Tyr Gly Pro Thr Asn Phe Ala Pro Ile Ile Asn His Val Ala Arg
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Phe Ala Ala Gln Ala Ala His Gln Gly Thr Ala Ser Gln Tyr Phe Met
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Glu Ala Val Val Arg Ala Ser Asn Leu Pro Met Ser Val Ile Ile Val
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Gly Val Gly Gly Ala Asp Phe Glu Ala Met Glu Gln Leu Asp Ala Asp
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Gly Gly Pro Leu His Thr Arg Ser Gly Gln Ala Ala Ala Arg Asp Ile
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Val Gln Phe Val Pro Tyr Arg Arg Phe Gln Asn Ala Pro Arg Glu Ala
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Leu Ala Gln Thr Val Leu Ala Glu Val Pro Thr Gln Leu Val Ser Tyr
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Lys Asp Pro Ala Gln Ala Pro Gln Ala
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Asn Phe Tyr Ser Val Phe Glu Gly Glu Leu Ser Asp Thr Ile Pro Val
35 40 45

Val His Ala Ser Ile Ala Gly Cys Arg Ile Ile Gly Arg Met Cys Val
50 55 60

Gly Asn Arg His Gly Leu Leu Val Pro Asn Asn Thr Thr Asp Gln Glu
65 70 75 80

Leu Gln His Ile Arg Asn Ser Leu Pro Asp Thr Val Gln Ile Arg Arg
85 90 95

Val Glu Glu Arg Leu Ser Ala Leu Gly Asn Val Thr Thr Cys Asn Asp
100 105 110

Tyr Val Ala Leu Val His Pro Asp Leu Asp Arg Glu Thr Glu Glu Ile
115 120 125

Leu Ala Asp Val Leu Lys Val Glu Val Phe Arg Gln Thr Val Ala Asp
130 135 140

Gln Val Leu Val Gly Ser Tyr Cys Val Phe Ser Asn Gln Gly Gly Leu
145 150 155 160

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Val His Pro Lys Thr Ser Ile Glu Asp Gln Asp Glu Leu Ser Ser Leu
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Leu Gln Val Pro Leu Val Ala Gly Thr Val Asn Arg Gly Ser Glu Val
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Ile Ala Ala Gly Met Val Val Asn Asp Trp Cys Ala Phe Cys Gly Leu
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Asp Thr Thr Ser Thr Glu Leu Ser Val Val Glu Ser Val Phe Lys Leu
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Pro Pro Thr Leu Pro Gly Asn Phe Leu Ile Ala Gly Ser Trp Ala Asn
50 55 60

Asp Val Arg Cys Trp Glu Val Gln Asp Ser Gly Gln Thr Ile Pro Lys
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Ala Gln Gln Met His Thr Gly Pro Val Leu Asp Val Cys Trp Ser Asp
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Asp Gly Ser Lys Val Phe Thr Ala Ser Cys Asp Lys Thr Ala Lys Met
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Trp Asp Leu Ser Ser Asn Gln Ala Ile Gln Ile Ala Gln His Asp Ala
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Pro Val Lys Thr Ile His Trp Ile Lys Ala Pro Asn Tyr Ser Cys Val
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Met Thr Gly Ser Trp Asp Lys Thr Leu Lys Phe Trp Asp Thr Arg Ser
145 150 155 160

Ser Asn Pro Met Met Val Leu Gln Leu Pro Glu Arg Cys Tyr Cys Ala
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Asp Val Ile Tyr Pro Met Ala Val Val Ala Thr Ala Glu Arg Gly Leu
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Ile Val Tyr Gln Leu Glu Asn Gln Pro Ser Glu Phe Arg Arg Ile Glu
195 200 205

Ser Pro Leu Lys His Gln His Arg Cys Val Ala Ile Phe Lys Asp Lys
210 215 220

Gln Asn Lys Pro Thr Gly Phe Ala Leu Gly Ser Ile Glu Gly Arg Val
225 230 235 240

Ala Ile His Tyr Ile Asn Pro Pro Asn Pro Ala Lys Asp Asn Phe Thr
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Phe Lys Cys His Arg Ser Asn Gly Thr Asn Thr Ser Ala Pro Gln Asp
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Cys Cys Phe Asn His Asn Gly Asn Ile Phe Ala Tyr Ala Ser Ser Tyr
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ttatgagcgc ctaccagcca ggccacccag ccgtgggagg aaggggcgt ggcaaggggt 1800
gggcacattg gtgtctgtgc gaaaggaaaa ttgacccgga agttcctgta ataaatgtca 1860
caataaaacg aatgaatg                                              1878
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<210> 10
<211> 431
<212> PRT
<213> Homo sapiens

<220>
<223> bone morphogenetic protein 7 (BMP7)

<400> 10
Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
1 5 10 15

Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
20 25 30

Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
35 40 45

Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
50 55 60

Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
65 70 75 80

Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
85 90 95

Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
100 105 110

Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
115 120 125

Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
130 135 140

Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
145 150 155 160

Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
165 170 175

Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
180 185 190

Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
195 200 205

Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
210 215 220

Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
225 230 235 240

His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
245 250 255

Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
260 265 270

```
Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
        275                 280                 285

Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
    290                 295                 300

Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
305                 310                 315                 320

Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
                325                 330                 335

Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
            340                 345                 350

Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
        355                 360                 365

Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
    370                 375                 380

Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
385                 390                 395                 400

Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
                405                 410                 415

Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
            420                 425                 430
```

<210> 11
<211> 1593
<212> DNA
<213> Homo sapiens

<220>
<223> guanine nucleotide binding protein (G protein),
alpha stimulating activity polypeptide 1 (GNAS)

<400> 11
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ccgccgccgc cgcagcccgg ccgcgccccg ccgccgccgc cgccgccatg ggctgcctcg 60
ggaacagtaa gaccgaggac cagcgcaacg aggagaaggc gcagcgtgag gccaacaaaa 120
agatcgagaa gcagctgcag aaggacaagc aggtctaccg ggccacgcac cgcctgctgc 180
tgctgggtgc tggagaatct ggtaaaagca ccattgtgaa gcagatgagg atcctgcatg 240
ttaatgggtt taatggagag ggcggcgaag aggacccgca ggctgcaagg agcaacagcg 300
atggtgagaa ggcaaccaaa gtgcaggaca tcaaaaacaa cctgaaagag gcgattgaaa 360
ccattgtggc cgccatgagc aacctggtgc cccccgtgga gctggccaac cccgagaacc 420
agttcagagt ggactacatc ctgagtgtga tgaacgtgcc tgactttgac ttccctcccg 480
aattctatga gcatgccaag gctctgtggg aggatgaagg agtgcgtgcc tgctacgaac 540
gctccaacga gtaccagctg attgactgtg cccagtactt cctggacaag atcgacgtga 600
tcaagcaggc tgactatgtg ccgagcgatc aggacctgct tcgctgccgt gtcctgactt 660
ctggaatctt tgagaccaag ttccaggtgg acaaagtcaa cttccacatg tttgacgtgg 720
gtggccagcg cgatgaacgc cgcaagtgga tccagtgctt caacgatgtg actgccatca 780
tcttcgtggt ggccagcagc agctacaaca tggtcatccg ggaggacaac cagaccaacc 840
gcctgcagga ggctctgaac ctcttcaaga gcatctggaa caacagatgg ctgcgcacca 900
tctctgtgat cctgttcctc aacaagcaag atctgctcgc tgagaaagtc cttgctggga 960
aatcgaagat tgaggactac tttccagaat ttgctcgcta cactactcct gaggatgcta 1020
ctcccgagcc cggagaggac ccacgcgtga cccgggccaa gtacttcatt cgagatgagt 1080
ttctgaggat cagcactgcc agtggagatg ggcgtcacta ctgctaccct catttcacct 1140
gcgctgtgga cactgagaac atccgccgtg tgttcaacga ctgccgtgac atcattcagc 1200
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```
gcatgcacct tcgtcagtac gagctgctct aagaagggaa cccccaaatt taattaaagc 1260
cttaagcaca attaattaaa agtgaaacgt aattgtacaa gcagttaatc acccaccata 1320
gggcatgatt aacaaagcaa cctttccctt cccccgagtg attttgcgaa acccccttt 1380
cccttcagct tgcttagatg ttccaaattt agaaagctta aggcggccta cagaaaaagg 1440
aaaaaaggcc acaaaagttc cctctcactt tcagtaaaaa taaataaaac agcagcagca 1500
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aaaaatcaaa ataaaaatta aatgtgagca aag                              1593
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<210> 12
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<223> guanine nucleotide binding protein (G protein),
alpha stimulating activity polypeptide 1 (GNAS)

<400> 12

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Met Gly Cys Leu Gly Asn Ser Lys Thr Glu Asp Gln Arg Asn Glu Glu
  1               5                  10                  15

Lys Ala Gln Arg Glu Ala Asn Lys Lys Ile Glu Lys Gln Leu Gln Lys
             20                  25                  30

Asp Lys Gln Val Tyr Arg Ala Thr His Arg Leu Leu Leu Leu Gly Ala
         35                  40                  45

Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His
     50                  55                  60

Val Asn Gly Phe Asn Gly Glu Gly Gly Glu Glu Asp Pro Gln Ala Ala
 65                  70                  75                  80

Arg Ser Asn Ser Asp Gly Glu Lys Ala Thr Lys Val Gln Asp Ile Lys
                 85                  90                  95

Asn Asn Leu Lys Glu Ala Ile Glu Thr Ile Val Ala Ala Met Ser Asn
            100                 105                 110

Leu Val Pro Pro Val Glu Leu Ala Asn Pro Glu Asn Gln Phe Arg Val
        115                 120                 125

Asp Tyr Ile Leu Ser Val Met Asn Val Pro Asp Phe Asp Phe Pro Pro
    130                 135                 140

Glu Phe Tyr Glu His Ala Lys Ala Leu Trp Glu Asp Glu Gly Val Arg
145                 150                 155                 160

Ala Cys Tyr Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln
                165                 170                 175

Tyr Phe Leu Asp Lys Ile Asp Val Ile Lys Gln Ala Asp Tyr Val Pro
            180                 185                 190

Ser Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe
        195                 200                 205

Glu Thr Lys Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val
    210                 215                 220
```

```
Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp
225                 230                 235                 240

Val Thr Ala Ile Ile Phe Val Val Ala Ser Ser Ser Tyr Asn Met Val
                245                 250                 255

Ile Arg Glu Asp Asn Gln Thr Asn Arg Leu Gln Glu Ala Leu Asn Leu
            260                 265                 270

Phe Lys Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Val Ile
        275                 280                 285

Leu Phe Leu Asn Lys Gln Asp Leu Leu Ala Glu Lys Val Leu Ala Gly
    290                 295                 300

Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Phe Ala Arg Tyr Thr Thr
305                 310                 315                 320

Pro Glu Asp Ala Thr Pro Glu Pro Gly Glu Asp Pro Arg Val Thr Arg
                325                 330                 335

Ala Lys Tyr Phe Ile Arg Asp Glu Phe Leu Arg Ile Ser Thr Ala Ser
            340                 345                 350

Gly Asp Gly Arg His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp
        355                 360                 365

Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln
    370                 375                 380

Arg Met His Leu Arg Gln Tyr Glu Leu Leu
385                 390
```

<210> 13
<211> 1439
<212> DNA
<213> Homo sapiens

<220>
<223> eukaryotic translation initiation factor 2,
subunit 2 beta (EIF2S2)

<400> 13
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ggggtgtcgt ttcctttcgc tgatgcaaga gcctagtgcg gtggtgggag aggtatcggc 60
aggggcagcg ctgccgccgg ggcctggggc tgacccgtct gacttcccgt ccgtgccgag 120
cccactcgag ccgcagccat gtctggggac gagatgattt ttgatcctac tatgagcaag 180
aagaaaaaga agaagaagaa gccttttatg ttagatgagg aaggggatac ccaaacagag 240
gaaacccagc cttcagaaac aaaagaagtg gagccagagc caactgagga caaggatttg 300
gaagctgatg aagaggacac taggaaaaaa gatgcttctg atgatctaga tgacttgaac 360
ttctttaatc aaaagaaaaa gaagaaaaaa actaaaaaga tatttgatat tgatgaagct 420
gaagaaggtg taaaggatct taagattgaa agtgatgttc aagaaccaac tgaaccagag 480
gatgaccttg acattatgct tggcaataaa aagaagaaaa agaagaatgt taagttccca 540
gatgaggatg aaatactaga gaaagatgaa gctctagaag atgaagacaa caaaaaagat 600
gatggtatct cattcagtaa tcagacaggc cctgcttggg caggctcaga aagagactac 660
acatacgagg agctgctgaa tcgagtgttc aacatcatga gggaaaagaa tccagatatg 720
gttgctgggg agaaaaggaa atttgtcatg aaacctccac aagtcgtccg agtaggaacc 780
aagaaaactt cttttgtcaa ctttacagat atctgtaaac tattacatcg tcagcccaaa 840
catctccttg catttttgtt ggctgaattg ggtacaagtg gttctataga tggtaataac 900
caacttgtaa tcaaaggaag attccaacag aaacagatag aaaatgtctt gagaagatat 960
atcaaggaat atgtcacttg tcacacatgc cgatcaccgg acacaatcct gcagaaggac 1020
```

acacgactct atttcctaca gtgcgaaact tgtcattcta gatgttctgt tgccagtatc 1080
aaaaccggct tccaggctgt cacgggcaag cgagcacagc tccgtgccaa agctaactaa 1140
tttgctaatc actgattttg caaagcttgt tgtggagatg tggctggaca ggtttgccat 1200
cagagtggat ataccgttgt attaaaaaca agataaaaaa gctgccaaga tttttggcga 1260
gtggttggtc tgaagtcctt gcaagacgct gatgctcaag ctgttgacat actcattgcc 1320
tactttaaca cctgtcagag aaacgtgata tggggtaagg aggtgctttt ttaaaatcgt 1380
tcatagactt ctgtaaaatg caagataaat taaagttatt ataacagtga ttctttcaa 1439

<210> 14
<211> 333
<212> PRT
<213> Homo sapiens

<220>
<223> eukaryotic translation initiation factor 2,
subunit 2 beta (EIF2S2)

<400> 14
Met Ser Gly Asp Glu Met Ile Phe Asp Pro Thr Met Ser Lys Lys Lys
1 5 10 15

Lys Lys Lys Lys Lys Pro Phe Met Leu Asp Glu Glu Gly Asp Thr Gln
20 25 30

Thr Glu Glu Thr Gln Pro Ser Glu Thr Lys Glu Val Glu Pro Glu Pro
35 40 45

Thr Glu Asp Lys Asp Leu Glu Ala Asp Glu Glu Asp Thr Arg Lys Lys
50 55 60

Asp Ala Ser Asp Asp Leu Asp Asp Leu Asn Phe Phe Asn Gln Lys Lys
65 70 75 80

Lys Lys Lys Lys Thr Lys Lys Ile Phe Asp Ile Asp Glu Ala Glu Glu
85 90 95

Gly Val Lys Asp Leu Lys Ile Glu Ser Asp Val Gln Glu Pro Thr Glu
100 105 110

Pro Glu Asp Asp Leu Asp Ile Met Leu Gly Asn Lys Lys Lys Lys Lys
115 120 125

Lys Asn Val Lys Phe Pro Asp Glu Asp Glu Ile Leu Glu Lys Asp Glu
130 135 140

Ala Leu Glu Asp Glu Asp Asn Lys Lys Asp Asp Gly Ile Ser Phe Ser
145 150 155 160

Asn Gln Thr Gly Pro Ala Trp Ala Gly Ser Glu Arg Asp Tyr Thr Tyr
165 170 175

Glu Glu Leu Leu Asn Arg Val Phe Asn Ile Met Arg Glu Lys Asn Pro
180 185 190

Asp Met Val Ala Gly Glu Lys Arg Lys Phe Val Met Lys Pro Pro Gln
195 200 205

Val Val Arg Val Gly Thr Lys Lys Thr Ser Phe Val Asn Phe Thr Asp
210 215 220

```
Ile Cys Lys Leu Leu His Arg Gln Pro Lys His Leu Leu Ala Phe Leu
225                 230                 235                 240

Leu Ala Glu Leu Gly Thr Ser Gly Ser Ile Asp Gly Asn Asn Gln Leu
                245                 250                 255

Val Ile Lys Gly Arg Phe Gln Gln Lys Gln Ile Glu Asn Val Leu Arg
            260                 265                 270

Arg Tyr Ile Lys Glu Tyr Val Thr Cys His Thr Cys Arg Ser Pro Asp
        275                 280                 285

Thr Ile Leu Gln Lys Asp Thr Arg Leu Tyr Phe Leu Gln Cys Glu Thr
    290                 295                 300

Cys His Ser Arg Cys Ser Val Ala Ser Ile Lys Thr Gly Phe Gln Ala
305                 310                 315                 320

Val Thr Gly Lys Arg Ala Gln Leu Arg Ala Lys Ala Asn
                325                 330
```

<210> 15
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<223> dynein light chain A2 (DNCL2A)

<400> 15
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cgcagaaagg cacaggactc gctaagtgtt cgctacgcgg ggctaccgga tcggtcggaa 60
atggcagagg tggaggagac actgaagcga ctgcagagcc agaagggagt gcagggaatc 120
atcgtcgtga acacagaagg cattcccatc aagagcacca tggacaaccc caccaccacc 180
cagtatgcca gcctcatgca cagcttcatc ctgaaggcac ggagcaccgt gcgtgacatc 240
gacccccaga acgatctcac cttccttcga attcgctcca agaaaaatga aattatggtt 300
gcaccagata aagactattt cctgattgtg attcagaatc caaccgaata agccactctc 360
ttggctccct gtgtcattcc ttaatttaat gccccccaag aatgttaatg tcaatcatgt 420
cagtggacta gcacatggca gtcgcttgga acccactcac accaatccag tgaccgtgtg 480
tgggctggcg gctcttctcc cccaccaacg gaacccctgt gtgcaccaac cttccccaga 540
gctccggagc gccctctcct cacttccagg ttttggagca agagcttgca ggaagcccgc 600
acccagcttc cttctgacct tcagttcact ttgtcgccct tggagaaagc tgtttttctt 660
taactaaaaa taaccaaaat gcttaaaaaa aaaaaaaaaa aa                    702
```

<210> 16
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<223> dynein light chain A2 (DNCL2A)

<400> 16
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Met Ala Glu Val Glu Glu Thr Leu Lys Arg Leu Gln Ser Gln Lys Gly
  1               5                  10                  15

Val Gln Gly Ile Ile Val Val Asn Thr Glu Gly Ile Pro Ile Lys Ser
            20                  25                  30
```

```
Thr Met Asp Asn Pro Thr Thr Thr Gln Tyr Ala Ser Leu Met His Ser
         35                  40                  45

Phe Ile Leu Lys Ala Arg Ser Thr Val Arg Asp Ile Asp Pro Gln Asn
     50                  55                  60

Asp Leu Thr Phe Leu Arg Ile Arg Ser Lys Lys Asn Glu Ile Met Val
 65                  70                  75                  80

Ala Pro Asp Lys Asp Tyr Phe Leu Ile Val Ile Gln Asn Pro Thr Glu
                 85                  90                  95
```

<210> 17
<211> 984
<212> DNA
<213> Homo sapiens

<220>
<223> proteasome subunit alpha-7 (PSMA7)

<400> 17

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cggcgccgag ggtggggcgc gggcgtagtg gcgccgggag tcgcgggtgc gcgcgggccg 60
tgagtgtgcg cttttgagag tcgcggcgga aggagcccgg ccgccgcccg ccggcatgag 120
ctacgaccgc gccatcaccg tcttctcgcc cgacggccac ctcttccaag tggagtacgc 180
gcaggaggcc gtcaagaagg gctcgaccgc ggttggtgtt cgaggaagag acattgttgt 240
tcttggtgtg gagaagaagt cagtggccaa actgcaggat gaaagaacag tgcggaagat 300
ctgtgctttg gatgacaacg tctgcatggc ctttgcaggc ctcaccgccg atgcaaggat 360
agtcatcaac agggcccggg tggagtgcca gagccaccgg ctgactgtgg aggacccggt 420
cactgtggag tacatcaccc gctacatcgc cagtctgaag cagcgttata cgcagagcaa 480
tgggcgcagg ccgtttggca tctctgccct catcgtgggt ttcgactttg atggcactcc 540
taggctctat cagactgacc cctcgggcac ataccatgcc tggaaggcca atgccatagg 600
tcggggtgcc aagtcagtgc gcgagttcct ggagaagaac tatactgacg aagccattga 660
aacagatgat ctgaccatta agctggtgat caaggcactc ctggaagtgg ttcagtcagg 720
tggcaaaaac attgaacttg ctgtcatgag gcgagatcaa tccctcaaga ttttaaatcc 780
tgaagaaatt gagaagtatg ttgctgaaat tgaaaaagaa aaagaagaaa acgaaaagaa 840
gaaacaaaag aaagcatcat gatgaataaa atgtctttgc ttgtaatttt taaattcata 900
tcaatcatgg atgagtctcg atgtgtaggc ctttccattc catttattca cactgagtgt 960
cctacaataa acttccgtat tttt                                        984
```

<210> 18
<211> 248
<212> PRT
<213> Homo sapiens

<220>
<223> proteasome subunit alpha-7 (PSMA7)

<400> 18

```
Met Ser Tyr Asp Arg Ala Ile Thr Val Phe Ser Pro Asp Gly His Leu
  1               5                  10                  15

Phe Gln Val Glu Tyr Ala Gln Glu Ala Val Lys Lys Gly Ser Thr Ala
             20                  25                  30

Val Gly Val Arg Gly Arg Asp Ile Val Val Leu Gly Val Glu Lys Lys
         35                  40                  45

Ser Val Ala Lys Leu Gln Asp Glu Arg Thr Val Arg Lys Ile Cys Ala
     50                  55                  60
```

```
Leu Asp Asp Asn Val Cys Met Ala Phe Ala Gly Leu Thr Ala Asp Ala
 65                  70                  75                  80

Arg Ile Val Ile Asn Arg Ala Arg Val Glu Cys Gln Ser His Arg Leu
                85                  90                  95

Thr Val Glu Asp Pro Val Thr Val Glu Tyr Ile Thr Arg Tyr Ile Ala
            100                 105                 110

Ser Leu Lys Gln Arg Tyr Thr Gln Ser Asn Gly Arg Arg Pro Phe Gly
        115                 120                 125

Ile Ser Ala Leu Ile Val Gly Phe Asp Phe Asp Gly Thr Pro Arg Leu
    130                 135                 140

Tyr Gln Thr Asp Pro Ser Gly Thr Tyr His Ala Trp Lys Ala Asn Ala
145                 150                 155                 160

Ile Gly Arg Gly Ala Lys Ser Val Arg Glu Phe Leu Glu Lys Asn Tyr
                165                 170                 175

Thr Asp Glu Ala Ile Glu Thr Asp Asp Leu Thr Ile Lys Leu Val Ile
            180                 185                 190

Lys Ala Leu Leu Glu Val Val Gln Ser Gly Gly Lys Asn Ile Glu Leu
        195                 200                 205

Ala Val Met Arg Arg Asp Gln Ser Leu Lys Ile Leu Asn Pro Glu Glu
    210                 215                 220

Ile Glu Lys Tyr Val Ala Glu Ile Glu Lys Glu Lys Glu Glu Asn Glu
225                 230                 235                 240

Lys Lys Lys Gln Lys Lys Ala Ser
                245
```

<210> 19
<211> 4713
<212> DNA
<213> Homo sapiens

<220>
<223> activity dependent neuroprotective protein (ADNP)

<400> 19
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cccccgagca cgccggcccc gcgcgcgcct cgaggccgag tcaaggtgtg agatgcacaa 180
tgcgaaacct aggccccagc ttttacacca tgatgcgcag ggttgtactt tttgtactga 240
actgataggt ggcctagtgg ttatgccctg tactaccatt ttgaggatct ggactccgtt 300
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gtcaacaatc ttggcagttt aagaaaagcc cggaaaactg tgaaaaaaat acttagtgac 420
attgggttgg aatactgtaa agaacatata gaagatttta aacaatttga acctaatgac 480
ttttatttga aaaacactac atgggaggat gtaggactgt gggacccatc acttacgaaa 540
aaccaggact atcggacaaa acctttctgc tgcagcgctt gtccattttc ctcaaaattc 600
ttctctgcct acaaaagtca tttccgcaat gtccatagtg aagactttga aaataggatt 660
ctccttaatt gcccctactg taccttcaat gcagacaaaa agactttgga aacacacatt 720
aaaatatttc atgctccgaa cgccagcgca ccaagtagca gcctcagcac tttcaaagat 780
aaaaacaaaa atgatggcct taaacctaag caggctgaca gtgtagagca agctgtttat 840
tactgtaaga agtgcactta ccgagatcct ctttatgaaa tagttaggaa gcacatttac 900
```

agggaacatt ttcagcatgt ggcagcacct tacatagcaa aggcaggaga aaaatcactc 960
aatggggcag tcccccttagg ctcgaatgcc cgagaagaga gtagtattca ctgcaagcga 1020
tgccttttca tgccaaagtc ctatgaagct ttggtacagc atgtcatcga agaccatgaa 1080
cgtataggct atcaggtcac tgccatgatt gggcacacaa atgtagtggt tccccgatcc 1140
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tcaatgagac tgggtctagg tggcaacgca ccagtttcca ttcctcaaca atctcagtct 1440
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aagatggccg cacacatgcg gatggttcac attgatgaag agatgggacc taaaacagat 1980
tctactttga gttttgattt gacattgcag cagggtagtc acactaacat ccatctcctg 2040
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aatcctccag ttcctccaaa gccacagcca aaggttcagg aaaaggcaga tatccctgta 2160
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ctttgctttt caatcctaaa aggacccata tctgatgcac ttgcacatca cttacgagag 2280
aggcaccaag ttattcagac ggttcatcca gttgagaaaa agctcaccta caaatgtatc 2340
cattgccttg gtgtgtatac cagcaacatg accgcctcaa ctatcactct gcatctagtt 2400
cactgcaggg gcgttggaaa gacccaaaat ggccaggata agacaaatgc accctctcgg 2460
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ttactgaaaa aacgaaagtt agatgatgat agtgattcac ccagcttctt tgaagagaag 2580
cctgaagagc ctgttgtttt agctttagac cccaagggtc atgaagatga ttcctatgaa 2640
gccaggaaaa gctttctaac aaagtatttc aacaaacagc cctatcccac caggagagaa 2700
attgagaagc tagcagccag tttatggtta tggaagagtg acatcgcttc ccattttagt 2760
aacaaaagga agaagtgtgt ccgtgattgt gaaaagtaca agcctggcgt gttgctgggg 2820
tttaacatga aagaattaaa taaagtcaag catgagatgg attttgatgc tgagtggcta 2880
tttgaaaatc atgatgagaa ggattccaga gtcaatgcta gtaagactgc tgacaaaaag 2940
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tagttttatc tttagttcaa caccatcatg gtggattcat ttataccatc taatatatga 4620
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catctaaata aattgctgta ttgtgcttaa tgt 4713

<210> 20
<211> 1102
<212> PRT
<213> Homo sapiens

<220>
<223> activity dependent neuroprotective protein (ADNP)

<400> 20
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1 5 10 15

Lys Thr Val Lys Lys Ile Leu Ser Asp Ile Gly Leu Glu Tyr Cys Lys
20 25 30

Glu His Ile Glu Asp Phe Lys Gln Phe Glu Pro Asn Asp Phe Tyr Leu
35 40 45

Lys Asn Thr Thr Trp Glu Asp Val Gly Leu Trp Asp Pro Ser Leu Thr
50 55 60

Lys Asn Gln Asp Tyr Arg Thr Lys Pro Phe Cys Cys Ser Ala Cys Pro
65 70 75 80

Phe Ser Ser Lys Phe Phe Ser Ala Tyr Lys Ser His Phe Arg Asn Val
85 90 95

His Ser Glu Asp Phe Glu Asn Arg Ile Leu Leu Asn Cys Pro Tyr Cys
100 105 110

Thr Phe Asn Ala Asp Lys Lys Thr Leu Glu Thr His Ile Lys Ile Phe
115 120 125

His Ala Pro Asn Ala Ser Ala Pro Ser Ser Ser Leu Ser Thr Phe Lys
130 135 140

Asp Lys Asn Lys Asn Asp Gly Leu Lys Pro Lys Gln Ala Asp Ser Val
145 150 155 160

Glu Gln Ala Val Tyr Tyr Cys Lys Lys Cys Thr Tyr Arg Asp Pro Leu
165 170 175

Tyr Glu Ile Val Arg Lys His Ile Tyr Arg Glu His Phe Gln His Val
180 185 190

Ala Ala Pro Tyr Ile Ala Lys Ala Gly Glu Lys Ser Leu Asn Gly Ala
195 200 205

Val Pro Leu Gly Ser Asn Ala Arg Glu Glu Ser Ser Ile His Cys Lys
210 215 220

Arg Cys Leu Phe Met Pro Lys Ser Tyr Glu Ala Leu Val Gln His Val
225 230 235 240

Ile Glu Asp His Glu Arg Ile Gly Tyr Gln Val Thr Ala Met Ile Gly
245 250 255

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His Thr Asn Val Val Val Pro Arg Ser Lys Pro Leu Met Leu Ile Ala
            260                 265                 270

Pro Lys Pro Gln Asp Lys Lys Ser Met Gly Leu Pro Pro Arg Ile Gly
        275                 280                 285

Ser Leu Ala Ser Gly Asn Val Arg Ser Leu Pro Ser Gln Gln Met Val
    290                 295                 300

Asn Arg Leu Ser Ile Pro Lys Pro Asn Leu Asn Ser Thr Gly Val Asn
305                 310                 315                 320

Met Met Ser Ser Val His Leu Gln Gln Asn Asn Tyr Gly Val Lys Ser
                325                 330                 335

Val Gly Gln Gly Tyr Ser Val Gly Gln Ser Met Arg Leu Gly Leu Gly
            340                 345                 350

Gly Asn Ala Pro Val Ser Ile Pro Gln Gln Ser Gln Ser Val Lys Gln
        355                 360                 365

Leu Leu Pro Ser Gly Asn Gly Arg Ser Tyr Gly Leu Gly Ser Glu Gln
    370                 375                 380

Arg Ser Gln Ala Pro Ala Arg Tyr Ser Leu Gln Ser Ala Asn Ala Ser
385                 390                 395                 400

Ser Leu Ser Ser Gly Gln Leu Lys Ser Pro Ser Leu Ser Gln Ser Gln
                405                 410                 415

Ala Ser Arg Val Leu Gly Gln Ser Ser Ser Lys Pro Ala Ala Ala Ala
            420                 425                 430

Thr Gly Pro Pro Pro Gly Asn Thr Ser Ser Thr Gln Lys Trp Lys Ile
        435                 440                 445

Cys Thr Ile Cys Asn Glu Leu Phe Pro Glu Asn Val Tyr Ser Val His
    450                 455                 460

Phe Glu Lys Glu His Lys Ala Glu Lys Val Pro Ala Val Ala Asn Tyr
465                 470                 475                 480

Ile Met Lys Ile His Asn Phe Thr Ser Lys Cys Leu Tyr Cys Asn Arg
                485                 490                 495

Tyr Leu Pro Thr Asp Thr Leu Leu Asn His Met Leu Ile His Gly Leu
            500                 505                 510

Ser Cys Pro Tyr Cys Arg Ser Thr Phe Asn Asp Val Glu Lys Met Ala
        515                 520                 525

Ala His Met Arg Met Val His Ile Asp Glu Glu Met Gly Pro Lys Thr
    530                 535                 540

Asp Ser Thr Leu Ser Phe Asp Leu Thr Leu Gln Gln Gly Ser His Thr
545                 550                 555                 560

Asn Ile His Leu Leu Val Thr Thr Tyr Asn Leu Arg Asp Ala Pro Ala
                565                 570                 575
```

Glu Ser Val Ala Tyr His Ala Gln Asn Asn Pro Pro Val Pro Pro Lys
580 585 590

Pro Gln Pro Lys Val Gln Glu Lys Ala Asp Ile Pro Val Lys Ser Ser
595 600 605

Pro Gln Ala Ala Val Pro Tyr Lys Lys Asp Val Gly Lys Thr Leu Cys
610 615 620

Pro Leu Cys Phe Ser Ile Leu Lys Gly Pro Ile Ser Asp Ala Leu Ala
625 630 635 640

His His Leu Arg Glu Arg His Gln Val Ile Gln Thr Val His Pro Val
645 650 655

Glu Lys Lys Leu Thr Tyr Lys Cys Ile His Cys Leu Gly Val Tyr Thr
660 665 670

Ser Asn Met Thr Ala Ser Thr Ile Thr Leu His Leu Val His Cys Arg
675 680 685

Gly Val Gly Lys Thr Gln Asn Gly Gln Asp Lys Thr Asn Ala Pro Ser
690 695 700

Arg Leu Asn Gln Ser Pro Ser Leu Ala Pro Val Lys Arg Thr Tyr Glu
705 710 715 720

Gln Met Glu Phe Pro Leu Leu Lys Lys Arg Lys Leu Asp Asp Asp Ser
725 730 735

Asp Ser Pro Ser Phe Phe Glu Glu Lys Pro Glu Glu Pro Val Val Leu
740 745 750

Ala Leu Asp Pro Lys Gly His Glu Asp Asp Ser Tyr Glu Ala Arg Lys
755 760 765

Ser Phe Leu Thr Lys Tyr Phe Asn Lys Gln Pro Tyr Pro Thr Arg Arg
770 775 780

Glu Ile Glu Lys Leu Ala Ala Ser Leu Trp Leu Trp Lys Ser Asp Ile
785 790 795 800

Ala Ser His Phe Ser Asn Lys Arg Lys Lys Cys Val Arg Asp Cys Glu
805 810 815

Lys Tyr Lys Pro Gly Val Leu Leu Gly Phe Asn Met Lys Glu Leu Asn
820 825 830

Lys Val Lys His Glu Met Asp Phe Asp Ala Glu Trp Leu Phe Glu Asn
835 840 845

His Asp Glu Lys Asp Ser Arg Val Asn Ala Ser Lys Thr Ala Asp Lys
850 855 860

Lys Leu Asn Leu Gly Lys Glu Asp Asp Ser Ser Ser Asp Ser Phe Glu
865 870 875 880

Asn Leu Glu Glu Glu Ser Asn Glu Ser Gly Ser Pro Phe Asp Pro Val
885 890 895

```
Phe Glu Val Glu Pro Lys Ile Ser Asn Asp Asn Pro Glu Glu His Val
            900                 905                 910

Leu Lys Val Ile Pro Glu Asp Ala Ser Glu Ser Glu Glu Lys Leu Asp
        915                 920                 925

Gln Lys Glu Asp Gly Ser Lys Tyr Glu Thr Ile His Leu Thr Glu Glu
    930                 935                 940

Pro Thr Lys Leu Met His Asn Ala Ser Asp Ser Glu Val Asp Gln Asp
945                 950                 955                 960

Asp Val Val Glu Trp Lys Asp Gly Ala Ser Pro Ser Glu Ser Gly Pro
                965                 970                 975

Gly Ser Gln Gln Val Ser Asp Phe Glu Asp Asn Thr Cys Glu Met Lys
            980                 985                 990

Pro Gly Thr Trp Ser Asp Glu Ser Ser Gln Ser Glu Asp Ala Arg Ser
        995                1000                1005

Ser Lys Pro Ala Ala Lys Lys Lys Ala Thr Met Gln Gly Asp Arg Glu
   1010                1015                1020

Gln Leu Lys Trp Lys Asn Ser Ser Tyr Gly Lys Val Glu Gly Phe Trp
1025                1030                1035                1040

Ser Lys Asp Gln Ser Gln Trp Lys Asn Ala Ser Glu Asn Asp Glu Arg
                1045                1050                1055

Leu Ser Asn Pro Gln Ile Glu Trp Gln Asn Ser Thr Ile Asp Ser Glu
            1060                1065                1070

Asp Gly Glu Gln Phe Asp Asn Met Thr Asp Gly Val Ala Glu Pro Met
        1075                1080                1085

His Gly Ser Leu Ala Gly Val Lys Leu Ser Ser Gln Gln Ala
   1090                1095                1100
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<210> 21
<211> 2427
<212> DNA
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 129 (C20orf129)
protein

<400> 21
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gattcaaagg ttgcctataa agcgggactg cacgccggtt tttgtccgag ggctgtcgag 120
tccgagcgcc gccatggctc tgctgtccga gggcctggac gaggtgcccg ccgcctgcct 180
gtcgccgtgc gggccgccca acccgaccga gctgttcagc gagtcacggc gcctggctct 240
ggaggagctg gtggcgggcg gccccgaagc cttcgcggcc ttcctgcgac gcgagcgcct 300
ggctcgtttc ctgaaccccg atgaggtgca cgccattctg cgcgcggcgg agaggccggg 360
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ctcttcgggc acctacttcc ccgagcagtc ggacctggag ccaccgctgt tggagcttgg 480
ctggcccgcc ttctaccagg gcgcctaccg cggcgccacg cgtgtcgaga cgcacttcca 540
gccccgcggc gctggcgaag gtggccccta cggctgcaag gacgctctgc gccagcagct 600
ccgctcggcg cgagaggtga ttgcagtggt catggacgtg ttcacagaca tcgacatctt 660
```

```
cagagacctg caagaaatat gcaggaaaca gggagttgct gtgtatatcc ttctggacca 720
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tggccaagtg gttgaacact ttgatctgga gttccgaatc ctgtatgccc agtccaagcc 1020
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<210> 22
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 129 (C20orf129)
protein

<400> 22

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Met Ala Arg Ala Cys Leu Ile Gln Arg Leu Pro Ile Lys Arg Asp Cys
  1               5                  10                  15

Thr Pro Val Phe Val Arg Gly Leu Ser Ser Pro Ser Ala Ala Met Ala
             20                  25                  30

Leu Leu Ser Glu Gly Leu Asp Glu Val Pro Ala Ala Cys Leu Ser Pro
         35                  40                  45

Cys Gly Pro Pro Asn Pro Thr Glu Leu Phe Ser Glu Ser Arg Arg Leu
     50                  55                  60

Ala Leu Glu Glu Leu Val Ala Gly Gly Pro Glu Ala Phe Ala Ala Phe
 65                  70                  75                  80

Leu Arg Arg Glu Arg Leu Ala Arg Phe Leu Asn Pro Asp Glu Val His
                 85                  90                  95
```

```
Ala Ile Leu Arg Ala Ala Glu Arg Pro Gly Glu Glu Gly Ala Ala Ala
            100                 105                 110

Ala Ala Ala Ala Glu Asp Ser Phe Gly Ser Ser His Asp Cys Ser Ser
        115                 120                 125

Gly Thr Tyr Phe Pro Glu Gln Ser Asp Leu Glu Pro Pro Leu Leu Glu
    130                 135                 140

Leu Gly Trp Pro Ala Phe Tyr Gln Gly Ala Tyr Arg Gly Ala Thr Arg
145                 150                 155                 160

Val Glu Thr His Phe Gln Pro Arg Gly Ala Gly Glu Gly Gly Pro Tyr
                165                 170                 175

Gly Cys Lys Asp Ala Leu Arg Gln Gln Leu Arg Ser Ala Arg Glu Val
            180                 185                 190

Ile Ala Val Val Met Asp Val Phe Thr Asp Ile Asp Ile Phe Arg Asp
        195                 200                 205

Leu Gln Glu Ile Cys Arg Lys Gln Gly Val Ala Val Tyr Ile Leu Leu
    210                 215                 220

Asp Gln Ala Leu Leu Ser Gln Phe Leu Asp Met Cys Met Asp Leu Lys
225                 230                 235                 240

Val His Pro Glu Gln Glu Lys Leu Met Thr Val Arg Thr Ile Thr Gly
                245                 250                 255

Asn Ile Tyr Tyr Ala Arg Ser Gly Thr Lys Ile Ile Gly Lys Val His
            260                 265                 270

Glu Lys Phe Thr Leu Ile Asp Gly Ile Arg Val Ala Thr Gly Ser Tyr
        275                 280                 285

Ser Phe Thr
    290
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<210> 23
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 52 (C20orf52)
protein

<400> 23
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cttacttccc ctgagccctt gggcccactt cccagcctac cgcttccgtc cccgcccgac 120
tcttgggcca gcgcctgggc ccacactttc ctatcccccg cagatgccgg tggccgtggg 180
tccctacgga cagtcccagc caagctgctt cgaccgtgtc aaaatgggct tcgtgatggg 240
ttgcgccgtg ggcatggcgg ccggggcgct cttcggcacc ttttcctgtc tcaggatcgg 300
aatgcggggt cgagagctga tgggcggcat tgggaaaacc atgatgcaga gtggcggcac 360
ctttggcaca ttcatggcca ttgggatggg catccgatgc taaccatggt tgccaactac 420
atctgtccct tcccatcaat cccagcccat gtactaataa aagaaagtct ttgagtaaaa 480
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aa   602

<210> 24
<211> 79
<212> PRT
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 52 (C20orf52)
protein

<400> 24
Met Pro Val Ala Val Gly Pro Tyr Gly Gln Ser Gln Pro Ser Cys Phe
1 5 10 15

Asp Arg Val Lys Met Gly Phe Val Met Gly Cys Ala Val Gly Met Ala
20 25 30

Ala Gly Ala Leu Phe Gly Thr Phe Ser Cys Leu Arg Ile Gly Met Arg
35 40 45

Gly Arg Glu Leu Met Gly Gly Ile Gly Lys Thr Met Met Gln Ser Gly
50 55 60

Gly Thr Phe Gly Thr Phe Met Ala Ile Gly Met Gly Ile Arg Cys
65 70 75

<210> 25
<211> 1685
<212> DNA
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 20 (C20orf20)
protein

<400> 25
ctcccgccgg gggctccttg ctcggccggg ccgcggccat gggagaggcc gaggtgggcg 60
gcgggggcgc cgcaggcgac aagggcccgg gggaggcggc caccagcccg gcggaggaga 120
cagtggtgtg gagccccgag gtggaggtgt gcctcttcca cgccatgctg ggccacaagc 180
ccgtcggtgt gaaccgacac ttccacatga tttgtattcg ggacaagttc agccagaaca 240
tcgggcggca ggtcccatcc aaggtcatct gggaccatct gagcaccatg tacgacatgc 300
aggcgctgca tgagtctgag attcttccat tcccgaatcc agagaggaac ttcgtccttc 360
cagaagagat cattcaggag gtccgagaag gaaaagtgat gatagaagag gagatgaaag 420
aggagatgaa ggaagacgtg gacccccaca atggggctga cgatgttttt tcatcttcag 480
ggagtttggg gaaagcatca gaaaaatcca gcaaagacaa agagaagaac tcctcagact 540
tggggtgcaa agaaggcgca gacaagcgga agcgcagccg ggtcaccgac aaagtcctga 600
ccgcaaacag caacccttcc agtcccagtg ctgccaagcg gcgccgcacg tagaccctca 660
gccctggtgg cggcagagaa gcgggcgagg cactgtggtc gctgaggggg ttggctgggt 720
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ggggaccgtg cagctgtcgg ctgatgagga ggcggccgcc ccagtgctga tggagatgcc 1560
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aaaaa 1685

<210> 26
<211> 204
<212> PRT
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 20 (C20orf20)
protein

<400> 26
Met Gly Glu Ala Glu Val Gly Gly Gly Gly Ala Ala Gly Asp Lys Gly
1 5 10 15

Pro Gly Glu Ala Ala Thr Ser Pro Ala Glu Glu Thr Val Val Trp Ser
20 25 30

Pro Glu Val Glu Val Cys Leu Phe His Ala Met Leu Gly His Lys Pro
35 40 45

Val Gly Val Asn Arg His Phe His Met Ile Cys Ile Arg Asp Lys Phe
50 55 60

Ser Gln Asn Ile Gly Arg Gln Val Pro Ser Lys Val Ile Trp Asp His
65 70 75 80

Leu Ser Thr Met Tyr Asp Met Gln Ala Leu His Glu Ser Glu Ile Leu
85 90 95

Pro Phe Pro Asn Pro Glu Arg Asn Phe Val Leu Pro Glu Glu Ile Ile
100 105 110

Gln Glu Val Arg Glu Gly Lys Val Met Ile Glu Glu Glu Met Lys Glu
115 120 125

Glu Met Lys Glu Asp Val Asp Pro His Asn Gly Ala Asp Asp Val Phe
130 135 140

Ser Ser Ser Gly Ser Leu Gly Lys Ala Ser Glu Lys Ser Ser Lys Asp
145 150 155 160

Lys Glu Lys Asn Ser Ser Asp Leu Gly Cys Lys Glu Gly Ala Asp Lys
165 170 175

Arg Lys Arg Ser Arg Val Thr Asp Lys Val Leu Thr Ala Asn Ser Asn
180 185 190

Pro Ser Ser Pro Ser Ala Ala Lys Arg Arg Arg Thr
195 200

<210> 27
<211> 3149
<212> DNA
<213> Homo sapiens

<220>
<223> chromosome 20 open reading frame 188 (C20orf188)
protein

<400> 27
gacatggcgg cggcgccggt agcggctggg tctggagccg gccgagggag acggtcggca 60
gccacagtgg cggcttgggg cggatggggc ggccggccgc ggcctggtaa cattctgctg 120
cagctgcggc agggccagct gaccggccgg ggcctggtcc gggcggtgca gttcactgag 180
acttttttga cggagaggga caaacaatcc aagtggagtg gaattcctca gctgctcctc 240
aagctgcaca ccaccagcca cctccacagt gactttgttg agtgtcaaaa catcctcaag 300
gaaatttctc ctcttctctc catggaggct atggcatttg ttactgaaga gaggaaactt 360
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gatgaaatgt ccaaggactg cttgagtatc ctgtataata cctgtgtctg tacagaggga 540
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gaaatgatcc gactagatga agtccccaat ctgagttcct tagtatccaa tttcgatcag 720
cagcagctcg ctaatttctg ccggattctg gctgtcacca tttcagagat ggatacaggg 780
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Val Thr Glu Glu Arg Lys Leu Thr Gln Glu Thr Thr Tyr Pro Asn Thr
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Tyr Ile Phe Asp Leu Phe Gly Gly Val Asp Leu Leu Val Glu Ile Leu
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Ala Thr Arg Lys Val Ser Glu Ser Thr Gly Thr Ala Ser Phe Leu Gln
305                 310                 315                 320

Glu Leu Glu Glu Trp Tyr Thr Trp Leu Asp Asn Ala Leu Val Leu Asp
                325                 330                 335

Ala Leu Met Arg Val Ala Asn Glu Glu Ser Glu His Asn Gln Ala Ser
            340                 345                 350

Ile Val Phe Pro Pro Pro Gly Ala Ser Glu Glu Asn Gly Leu Pro His
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Thr Ser Ala Arg Thr Gln Leu Pro Gln Ser Met Lys Ile Met His Glu
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Ile Met Tyr Lys Leu Glu Val Leu Tyr Val Leu Cys Val Leu Leu Met
385                 390                 395                 400

Gly Arg Gln Arg Asn Gln Val His Arg Met Ile Ala Glu Phe Lys Leu
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Ile Pro Gly Leu Asn Asn Leu Phe Asp Lys Leu Ile Trp Arg Lys His
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Ser Ala Ser Ala Leu Val Leu His Gly His Asn Gln Asn Cys Asp Cys
        435                 440                 445

Ser Pro Asp Ile Thr Leu Lys Ile Gln Phe Leu Arg Leu Leu Gln Ser
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Ser Ser Phe Arg Phe Trp Gln Ala Arg Ala Val Glu Ser Phe Leu Arg
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Gln Val Asp Met Lys Val Ala Glu Val Leu Ser Glu Cys Arg Leu Leu
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Ala Tyr Ile Ser Gln Val Pro Thr Gln Met Ser Phe Leu Phe Arg Leu
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705                 710                 715                 720

Tyr Pro Gly Phe Leu Leu Asn Asn Phe His Asn Leu Leu Arg Phe Trp
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Gln Gln His Tyr Leu His Lys Asp Lys Asp Ser Thr Cys Leu Glu Asn
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Ser Ser Cys Ile Ser Phe Ser Tyr Trp Lys Glu Thr Val Ser Ile Leu
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Leu Asn Pro Asp Arg Gln Ser Pro Ser Ala Leu Val Ser Tyr Ile Glu
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Glu Pro Tyr Met Asp Ile Asp Arg Asp Phe Thr Glu Glu
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